

STIC-Biotech/ChemLib

54329

From: Baum, Stuart
Sent: Tuesday, January 29, 2002 6:35 PM
To: STIC-Biotech/ChemLib
Subject: Sequence Search....thank you

Please do a sequence search for:
SEQ ID NO:1
SEQ ID NO:2

Please search these sequences against the protein data base only...thanks

EXAMINER # 78896
DATE:1/29/02

SERIAL NUMBER:08/763704

MAIL BOX ROOM: CM1 9E12
OFFICE ROOM # CM1 9D06

RESULTS FORMAT: PAPER

THANKS...Stuart

Stuart F. Baum Ph.D
Art Unit 1638
CM1 9D06
(703) 305-6997
stuart.baum@uspto.gov

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 1/30/02
Date Completed: 1/31/02
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: 2 - Reverse to
AA Sequences: AA
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST(where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: 04
WWW/Internet: _____
Other (specify): _____



39 ZEA2_MALZF:


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17 rValAlaThrAlaThrIlePheProGlnCysSerGlnAlaProGlnAlaLeu
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104	InGInLeuLeuProPheSerGInGInLeuAlaThrAlaTyrSerGInGInGln 120
999	C^AAUUCGUHRC^CAUUC^AAA^CAA^GGG^AGC^AGC^AUACAACUCU^AUUG^UAUAGU 1048
121	GInPheLeuProPheAsnGInLeuAlaAlaLeuAsnProSerAlaTyrPh 137
1049	A^AAC^AAC^AAC^AUA^UAC^CAUUC^AACC^AGC^AGC^UAG^UGUGUGACGCCUG 1098
137	eGInGInGInGInLeuLeuProPheSerGInLeuAlaA^aAlaSerArgA 154
1099	GUUGCGUHCURGC^ACAC^AACA^CAUUCGUUGCGUGUUCUACCGUGCACACUGGAG 1148
154	IaSeSerPheLeuThrGInGInGInLeuLeuProPheTyrGInGInPheAla 170
1149	C^UAA^CGUGUGAC^CCGCUUUA^AACCGUC^CAACA^AUUGUGUGCC^CAUUCGACCA 1198
171	AlaAsnProAlaThrLeuLeuGInLeuGInGInLeuLeuProPheValGI 187
1199	A^CHRG^GHUUGCA^AAACCC^ACGAGUGUCUACCAAC^ACGCC^CAUCAUUGGUG 1248
187	UleuAlaLeuThrHisProAlaIaSerTyrGInGInProIleIleGlyC 204
1249	GUUGCGUHCURUB 1259
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seq_name:	sp_plant :Q06771
seq_id:	Q06771 PRELIMINARY; PRT; 266 AA.
AC	Q06771;
RD	01-NOV-1996 (TRMBUREL_01, Created)
DT	01-NOV-1996 (TRMBUREL_01, Last sequence update)
RX	01-JUN-2001 (TRMBUREL_17, Last annotation update)
DE	ALPHA-COXIXIN PRECURSOR (ALPHA PROLAMIN).
GN	ALPHA-4B.
OC	Coix lachryma-jobi (Jobs Tears).
CC	Fumarietia; Viridiplantae; Streptophyta, Embryophyta; Tracheophyta;
CC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
CC	Panicoidae; Andropogoneae; Coix.
OX	NCBI_TaxID:4505;
RA	[1]
RP	SEQUENCE FROM R.A.
RE	STRAIN CV. ARLAY; TISSUE: SEEDLING;
RA	MEDLINE 94222476; PubMed 8467075;
RA	©Johnson L.M.M., Leite A., Yunes J.A., Targon M.L.P.N.,
RA	de Souza Filho G.A., Artuda P.;
RT	*Sequence analysis of 22 kDa-pI alpha-coixin genes and their
RT	comparison with homologous zein and kafirin genes reveals highly
KL	conserved protein structure and regulatory elements.*;
PL	Plant Mol. Biol., 21:765-778(1993).
CC	-P- FUNCTION: SEED STORAGE PROTEIN. SERVES AS A SOURCE OF NITROGEN,
CC	CARBON, AND SULFUR FOR THE YOUNG DEVELOPING SEEDLING.
CC	-I- SUBCELLULAR LOCATION: PROTEIN BODIES INSIDE VACUOLES.
CC	-S- SIMILARITY: TO MAIZE ZEIN AND SOYBEAN KAFIRIN
DR	EMBL: X64114; CAA44827.1; ..
DR	RefSeq: 11671; Colila:1411;11671.
DR	InterPro: IPR002540; Zein; 1.
KW	Plam; PPO1539; Zein; 1.
FT	Seed storage protein; Multigene family; Signal; Repeat.
FT	SIGNAL 1 21 POTENTIAL..
FT	CHAIN 22 266 ALPHA-COXIXIN.
FT	DOMAIN 58 257 10 X APPROXIMATE TANDEM REPEATS..
FT	REPEAT 58 85 1.
FT	REPEAT 86 100 2.
FT	REPEAT 101 113 3.
FT	REPEAT 114 132 4.
FT	REPEAT 133 156 5.
FT	REPEAT 157 175 6.


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Ratio:      2.670
Percent_Similarity: 64.966
Length:     294
Gaps:       12
Percent_Identity: 48.299

alignment_block:

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509 UCUCUCACGGGATGCAUHUUGCGCACAAUGUCACAAAGGUCCU 551
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17 ThrThrTrpAlaValIleIleProClnCysSerLeuAlaProAsnAlaI 34
552 . . . AUAGCUHUCGUCUUGCGCGCAUACGUCUCACCACGAGAGUCUUCAGUA 599
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34 IleSerGlnSorLeuProPro . . . LeuThrPro MetCly 46
600 UUGAAAAAUGCACAUGUUCUUAUGGCUACAGGAUGCAACAGGCACUUGGAGC 649
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47 PheGlnHisProAlaLeuGlnAlaTyrArgLeuGlnGlnAlaLeuAlaAs 63
650 AGGCAACACUACGUUUAUACAGCUUGUCUCCACCAUUCACAGCGCCU 699
||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
63 nSorIle LeuGlnGlnProPheAlaGlnL 73
700 UACAGAGUUAUUCUUUGUGCAUUGGACAAACAAACAGCGGCACAA 749
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74 euGInGInGInSerSerGlyHisLeuThrValGInThrIleAlaAlaGln 89
750 CAA CUACAAACATCTGTCGACGCAACCCU 778
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90 GlnGlnGlnGlnPheLeuProValAlaLeuSerIleIleAlaLeuAlaLysPr 106
779 UCUCUCUUAUCUCAGCAACACACAGUA GUHHGUGUCAU 819
||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
106 oAlaAlaTyrLeuGlnGlnGlnGlnLeuAlaSerAsuProLeuAlaLeuV 123
820 UCUHGGCACAAAACAUACAGGACCAACAAACUACAAACAACTUCUG 863
||| : ||||| : ||||| : ||||| : ||||| : ||||| :
123 alAshAsuAlaAlaTyrGlnGlnGlnGlnGlnGlnGlnValLeuProVal 139
864 CUAGCAAACTUUGGUGGCCUACUCAGCAGCAACA 898
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156 MetAlaAsuProAlaAlaTyrLeuGlnGlnGlnGln 156

[illegible]

X


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161  Ser Ser Pro Leu Ala Val Val Asn Ala Pro Thr Tyr Leu Glu Glu 178
568  ....CAACAAAGUUCUUCUUA...UUUAAAGCAAUUGGACGACACUGAAC 606
178  Inu Leu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu 194
607  CCACAGUGCUUAUUUGAAGACAGCAAAUAUAUAUACCAUHUAGCCACGCUAGC 656
195  Pro Ala Ala Tyr Leu Glu Glu Glu Glu Glu Glu Glu Glu Glu 209
657  UGAAGACAAACCAUUGCUUUCUUGUAGACACAGCAACACAGUUGGUGUGCUUUCU 706
209  rV41SerAsnSerAlaAlaTyrLeuGluGluGluGluGluGluGluGluGlu 225
707  AGCAGACAUUUUACGCGCAACGCG...GCAACCCUUCUUAACACUUA 750
225  snProLeuAlaValAlaAlaAsnProLeuValAlaAlaPheLeuGluGluGlu 241
751  CAAUUUGUAGCCUUGUGUCUACACUUGCUUUGAAGAGACCGAGGCGGCUUGUA 800
242  GluLeuLeuProTyrAsnGluPheSerLeuMetAsnProAlaLeuLysTr 258
801  CCAACAACACAAUAUUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGG 831
258  polInuProIleValGlyGlyAlaIlePhe 268
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[illegible]

100

seq_documentation_lock:
 19K zein precursor (clone M6) - maize
 Species: *Zea mays* (maize)
 #Sequence revision: 19 May 1989 #text_change: 0
 #Date: 19-May-1989
 C.Accession: A22831
 R.Viotti, A.; Curro, G.; Vitale, A.; Salda, E.
 EMBO J. 4, 1103-1110, 1985
 A.Title: Each zein gene class can produce polypeptides of different sizes.
 A.Reference number: A91003
 A.Accession: A22831
 A.Molecule type: mRNA
 A.Residues: 1-240 aa/aa
 A.Note: the authors translated the codon GGU for residue 106 as Ala. and GGU
 as Superfamily: zein

[illegible][illegible]

Seed Name: pir2:A22831


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550 ACUGGCUUAUCUCACAGCAACAACAAACUUGUCACUUAUAAACAAUUGCGCGC 599
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600 ACUGAACCCGCGUGGCUUAUUGGACGACGACGACAAAUACUACUACCAUUGAGCC 649
      :::::
156 AlaAsnSerAlaAlaTyrLeuGlnGlnGlnGlnLeuLeuProPheSerG 173
      :::::
650 ACUUAAGCUGCAGCAGCAACCGUGGUGGUGGUGGACACACACACAGUUGGUG 699
      :::::
174 IleuAlaAspValSerProAlaAlaPheLeuThrGlnGlnGlnLeuLeu 189
      :::::
700 CUGUUGUAACAGCAGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGG 749
      :::::
190 ProPheTyrLeuIleAlaMetProAsnAlaTyrThrLeuLeuGlnLeuG 206
      :::::
750 ACUAUUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGG 799
      :::::
206 GlnLeuLeuProPheAsnGlnLeuAlaLeuThrAsnSerThrValPheT 223
      :::::
800 ACUAACAAACAAUACUUAUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGG 831
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224 TyrGlnGlnProIleIleGlyGlyAlaLeuPhe 233
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509 UGUGUGAGCGGAGGCAUUUUUGCGAAGUGUACAAAGATTCUUAUAGUUU 658
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559 CCUUCUUGCGCCCAUACCUUCACAGCAGGAGUGUUCUAAUAGUGCAAAAU 608
34 erLeuLeuProProTyLeuSerSerAlaValSerSerValICysGluAsn 69
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51 ProLieLeuGlnProTyArgLieGlnGlnAlaLieAlaLieAlaLieLie 67
659 ACCUUAUACACCUUGUUGUUGUCCCAACAAUUAUACAGUUAUUAUUAAGU 708
67 uProLeuSerProLeuPheLeuGlnGlnLieSerAlaLieLeu 81
709 UAGCUUUGUGUGCAUUAUUGUGCAGAAAAAUAGAGGCAAAAUUAUA 758
81 81
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100 102
85 oLeuValHisLeuLeuAlaGlnAsnLieArgAlaGlnGlnLeuGlnLie 102
859 UCGUGUGUAGCAAAACCUUGUGUGUUAUUAUUAUUAUUAUUAUUAUUA 908
102 euValLeuAlaAsnLeuAlaLieTySerGlnGlnGlnGlnGlnPheLeuPro 118
909 UUCAACAAACUAGCGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 958
119 PheAsnGlnLeuGlySerLeuAsnSerAlaSerTyLeuGlnGlnGlnGln 135
959 ACUACUACUUAUACGCCAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 1008
135 h.....LeuProPheSerGlnLeuArgAlaGlnAlaTyProGlnGlnPheLeuP 151
1009 CAUUCAAACCAACUGGAGCAUUGAGUAGUAGUAGUAGUAGUAGUAGUAGU 1058
151 roPheAsnGlnLeuAlaAlaLeuAsnSerProAlaTyLeuGlnGlnGlnGln 167
1059 CAACUACUACUACUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 1108
168 GlnLeuLeuProPheSerGlnLeuAlaGlnValSerProAlaLiePheLe 184
1109 GACAAACAAACUUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUGUG 1158
184 uThrGlnProGlnLeuLeuProPheTyGlnHisValAlaProAsnAlaGln 201
1159 GCACUUCUUAUACUAGCACAUAUUGUGUGUGUGUGUGUGUGUGUGUGUG 1208
201 TyThrLeuLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 217
1209 ACAAAACCAAGCAUGUGUGUACAAACAAACCAAGCAAGCAAGCAAGCAAG 1258
218 ThrAsnProAlaValPheTyGlnGlnGlnProLieLieGlyGlyAlaLeuPhe 234
1259 U 1259
234 e 234

seq name: SwissProt_39;ZEA5_MALZF

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seq_documentation_block:
D 7E45 M41FE STANDARD:
PRI: 234 AA.
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P08416;
01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
ZFIN-ALPHA PEPPERSON (19 KDA) (CLONE GZ19A811).

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1159 GACACCTCTCTACAAACUGCAACAAUUGUGCCAUUGGACCAACUUGGCUUG 1208
1160 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
201 1yhrLeuLeuGlnLeuGlnLeuLeuLeuLeuLeuLeuLeuLeuLeu 217
1209 ACAAAACCAAGTAGGUGUUCUACCAACCAACCAUUGUGUGUGGUCUUCU 1258
1210 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
218 ThrAsnLeuAlaAlaPheTyrGlnGlnProIleLeuGlyAlaLeu 234
1259 U 1259
1260 |
234 c 234

_q_name: SwissProt_39:ZEA4_MAIZE
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ZEA4_MAIZE STANDARD; PRT; 234 AA.
006675;
01-JAN-1988 (Rel. 06, Created)
01-JUN-1988 (Rel. 06, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
ZEA4_MAIZE PRESEQUOR (19 KDA) (CLONE 19B1).
Zea mays (Maize).
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
NCBI_TaxID 4577;
[1]
SEQUENCE FROM N.A.
MEDLINE 86059564; PubMed 299157;
Marks M.D., Lindell J.S., Larkins B.A.:
"Nucleotide sequence analysis of zein mRNAs from maize endosperm ";
J. Biol. Chem. 260:16451-16459(1985).
-1- FUNCTION: ZEINS ARE MAJOR SEED STORAGE PROTEINS.
-1- MISCELLANEOUS: THE ALPHA ZEINS OF 19 KDA AND 22 KDA ACCOUNT FOR
70% OF THE TOTAL ZEIN FRACTION. THEY ARE ENCODED BY A LARGE
MULTIGENE FAMILY.
-1- MISCELLANEOUS: STRUCTURALLY, 22K AND 19K ZEINS ARE COMPOSED OF
NINE ADJACENT, TOPOLOGICALLY ANTIPARALLEL HELICES CLUSTERED WITHIN
A DISTORTED CYLINDER.
-----
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C	EMBL	M12144	AAA3527.1	-
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R	MalzODB	58096	-	
R	InterPro	IPR002530	Zein	
R	Plant	PP01559	Zein; 1	
R	Seed storage protein	Repeat	Multigene family; Signal	
W	SIGNAL	1	21	
T	CHAIN	22	214	ZEIN-ALPHA
T	SEQUENCE	234 AA	254-45 MW	A641FE13961136A2 NC64

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Quality:	1029.50	length:	267
Ratio:	4.515	Gaps:	2
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US-08-763-704A-2 x ZEN4_MAIZE ...
Align seq i/1 to ZEN4_MAIZE from 1 to 234

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459 AUGGACGCAAAAUUUUUGCCUCAUUUAUGUCCUUGGUCUUUCUGCAAG 508
1 Met Ala Ala Val Tyr Phe Cys Leu Met Leu Cys Val Ser Ala Leu 17


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|||||
67 UProLeuSerProLeuPheLeuGlnGlnSerAlaLeuLeuGlnGlnL 84
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117 oLeuValHisLeuLeuAlaGlnAsnIleArqAlaGlnIndeuGlnGlnL 134
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909 URKAATCAACUAGCUGCGAUUCAACUCUGCGCGCUAUUUGCACGAACAACA 958
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151 PheAsnGln..... 153
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154 .....GlnLeuAlaAlaAlaTyrProArgGlnPheLeuPr 165
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1009 CAUUCACACACGCGACGACGACGACGACGACGACGACGACGACGACGACGAC 1058
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pub676;
01-JAN-1988 (rel. 06, Created)
01-JAN-1988 (rel. 06, last sequence update)
01-JUN-1994 (rel. 29, last annotation update)
ZEIN-ALPHA PRECURSOR (19 KDA) (CLONE 19C1).
Zea mays (Maize).
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyte; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
NCBI_TaxID: 4577;
111
SEQUENCE FROM N.A.
MEDLINE: 86059563; PubMed-2959457;
Marks M.D., Lindell J.S., Larkins B.A.;
"Nucleotide sequence analysis of zein mRNAs from maize endosperm.";
J. Biol. Chem. 260:16451-16459(1985).
1- FUNCTION: ZEINS ARE MAJOR SEED STORAGE PROTEINS.
1- MISCELLANEOUS: THE ALPHA ZEINS OF 19 KDA AND 22 KDA ACCOUNT FOR
70% OF THE TOTAL ZEIN FRACTION. THEY ARE ENCODED BY A LARGE
MULTIGENE FAMILY.
1- MISCELLANEOUS: STRUCTURALLY, 22K AND 19K ZEINS ARE COMPOSED OF
NINE ADJACENT, TOPOLOGICALLY ANTIPARALLEL HELICES CLUSTERED WITHIN
A DISTORTED CYLINDER.
-----
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51 ProlLeuLeuProTyrAlaIleGlnAlaIleAlaIleAlaGlyIleLeu 67
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659 ACCUUUAACACGCGGGGCGGCCTCCAAACAACAUCAACGCCGUAAUACAGCU 708
|||||
67 UProLeuSerProLeuGlnGlnSerAlaLeuLeuGlnGlnL 84
|||||
709 UACGCHHGCGCAUUDUUGGACACAAAACAACAGCGGCACACACAAUACAAA 758
|||||
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759 CAACUGCGGCAACCAACGCGCGGCGUACUCUACAGCAACAGCAGUACC 808
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101 GlnLeuValLeuAlaAsnLeuAlaAlaTyrSerGlnGlnGlnGlnLeuPr 117
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809 UHHGCGCGCAUUDUUGGACACAAAACAACAGCGGCACACAAUACAAAC 858
|||||
117 oLeuValHisLeuLeuAlaGlnAsnIleArqAlaGlnIndeuGlnGlnL 134
|||||
859 UCUGGCGUAGCAAACTHGGCGGCGUACUCUACAGCAACAGCAGUUDUGCCA 908
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134 euValLeuAlaAsnIndeuAlaAlaTyrSerGlnGlnGlnGlnPhelLeuPr 150
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151 PhcAsnGln..... 153
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p06676;
01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, last sequence update)
01-JUN-1994 (Rel. 29, last annotation update)
ZEIN-ALPHA PRECURSOR (19 KDA) (CLONE 19C1).
Zein mays (Maize).
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
NCBI_TaxID: 4577;
111
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MEDLINE: 86059563; PubMed-2959457;
Marks M.D., Lindell J.S., Larkins B.A.;
"Nucleotide sequence analysis of zein mRNAs from maize endosperm.";
J. Biol. Chem. 260:16451-16459(1985).
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70% OF THE TOTAL ZEIN FRACTION. THEY ARE ENCODED BY A LARGE
MULTIGENE FAMILY.
1- MISCELLANEOUS: STRUCTURALLY, 22K AND 19K ZEINS ARE COMPOSED OF
NINE ADJACENT, TOPOLOGICALLY ANTIPARALLEL HELICES CLUSTERED WITHIN
A DISTORTED CYLINDER.
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p04702:
13-AUG-1987 (Ref. 05, Created)
14-AUG-1987 (Ref. 05, Last sequence update)
01-JUN-1994 (Ref. 29, Last annotation update)
ZEA6_MAIZE: PROTEIN (19 KDA) (CLONE M6).
Zea mays (Maize).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Panicoideae; Andropogoneae; Zea.
NCBI_TaxID=4577;
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SEQUENCE FROM N.A.
VICTI A., Cairo G., Vitale A., Sala E.
"Each zein gene class can produce polypeptides of different
EMBO J. 4:1103-1110(1985)
-1- FUNCTION: ZEINS ARE MAJOR SEED STORAGE PROTEINS.
-1- MISCELLANEOUS: THE ALPHA ZEINS OF 19 KDA AND 22 KDA A
-1- 70% OF THE TOTAL ZEIN FRACTION. THEY ARE ENCODED BY A

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seq_documentation_block:
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01-JAN-1988 (rel. 06, created)
01-JAN-1988 (rel. 06, last sequence update)
01-JUN-1994 (rel. 29, last annotation update)
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Panicoideae: Andropogoneae: Zea.
NCBI_TaxID 4577;
111
SEQUENCE FROM N.A.
MEDLINE R6059563; PubMed-2999157;
Marks M.D., Lindell J.S., Larkins B.A.;
"Nucleotide sequence analysis of zein mRNAs from maize endosperm.";
J. Biol. Chem. 260:16451-16459(1985).
1- FUNCTION: ZEINS ARE MAJOR SEED STORAGE PROTEINS.
1- MISCELLANEOUS: THE ALPHA ZEINS OF 19 KDA AND 22 KDA ACCOUNT FOR
70% OF THE TOTAL ZEIN FRACTION. THEY ARE ENCODED BY A LARGE
MULTIGENE FAMILY.
1- MISCELLANEOUS: STRUCTURALLY, 22K AND 19K ZEINS ARE COMPOSED OF
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or send an email to license@isb-sib.ch.)
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EMBL: M12145; AAA33530.1; -
PIR: R24557; Z1ZM92.
Matzchr: 58096; Zein.
InterPro: IPR002530; Zein.
Plant: PF01559; Zein; 1.
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1 PRIOR APPLICATION DATA:
 2 APPLICATION NUMBER: 07/643,237
 3 FILING DATE: 18-JAN-1991
 4 TELECOMMUNICATION INFORMATION:
 5 TELEPHONE: 202-628-5197
 6 TELEFAX: 202-747-4528
 7 INFORMATION FOR SEQ ID NO: 6:
 8 SEQUENCE CHARACTERISTICS:
 9 LENGTH: 801 amino acids
 10 TYPE: amino acid
 11 STRANDEDNESS: single
 12 TOPOLOGY: linear
 13 MOLECULE TYPE: protein
 14 US 07-906 349A-6

alignment_scores:

Quality: 145.00 Length: 317
 Ratio: 1.249 Gaps: 14
 Percent Similarity: 46.909 Percent Identity: 20.505

alignment block:

US-08-763-704A-2:rev x US 07-906 349A-6

Align seq 1/1 to: US-07-906-349A-6 from: 1 to: 801

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407 T 407
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597 s 597

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seq_name: rev_2:3:4: 643,237A C-OMM, prepared on 01-01-02

seq_documentation block:

1 Sequence: 15, Applicant: 02/29/2005, 15
 2 Patent No.: 6015882
 3 GENERAL INFORMATION:
 4 APPLICANT: PETERSEN, CAROLYN
 5 APPLICANT: LEECH, JAMES
 6 APPLICANT: NELSON, RICHARD, C.
 7 APPLICANT: GUT, JIM
 8 TITLE OF INVENTION: VACCINES, ANTIBODIES, PEPTIDES, AND TREATMENT OF HIV INFECTION
 9 TITLE OF INVENTION: INFECTIONS
 10 FILE REFERENCE: 460,194 (BV)
 11 CURRENT APPLICATION NUMBER: 05/790,951B
 12 CURRENT FILING DATE: 1997-08-14
 13 EARLIER APPLICATION NUMBER: 08/416,761
 14 EARLIER FILING DATE: 1995-04-04
 15 NUMBER OF SEQ ID NOS: 15
 16 SOFTWARE: Patent In Vnt, 2.0
 17 SEQ ID NO: 15
 18 LENGTH: 249
 19 TYPE: PRT
 20 ORGANISM: cytospodium parvum
 21 FEATURE:
 22 OTHER INFORMATION: mutant variant of SEQ ID NO: 15
 23 US 08-700 651 15

alignment_scores:

Quality: 145.00 Length: 317
 Ratio: 1.249 Gaps: 14
 Percent Similarity: 45.660 Percent Identity: 20.544

alignment block:

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 Align seq 1/1 to: US 08-700 651 15 from: 1 to: 249
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1  II .....Gly 72
71  ys.....Gly 72
898 TGTGCTGCTGACAGTACGATAGCAAGGTTTGTATACACAGAGTTGTGTGAG 849
1  IIIII ..... 1
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648 CTGAGATGCTGCTGTGATCTGT 625
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